



SEQUENCE LISTING

<110> BATHE, BRIGITTE
KREUTZER, CAROLINE
MARX, ACHIM
PFEFFERLE, WALTER

<120> NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE
LUXS GENE

<130> MAS/21123/280106

<140> 09/824,551

<141> 2001-04-04

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1902

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (342) .. (1610)

<223> luxS-Gen

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cggtgcgttc gaccgcgggc atcgcgctga tgggaaggcc gtcagtaatt acttccgggg 180
ctgcctcggg ggtggtctct ggggttgctt caggttcgcg cggggtacaa gcggtgagca 240
tgatggaagc agcgaggata gtaggtaatg tacgacgcat gcagtcaagc ctagatcgtg 300
tgtcggaaac cggacgcaat gagctcgatg ttgaaaccct t gtg aag aag ggg aat 356
Met Lys Lys Gly Asn
1 5

caa ccg ggc gcg atg agc tat cgc aac agt atc cac att ttg aca gcc 404
Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala
10 15 20

tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc cgc ctg acg ctg ccg 452
Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro
25 30 35

atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac 500
Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr
40 45 50

AI
omit

ttc tat gga tca acc aaa cgc gta gat ttg agc cac ggc atg cag ctg 548
 Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu
 55 60 65

ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att ttt atg gtg ccg atc 596
 Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Pro Ile
 70 75 80 85

gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg ttt ttc ctc tat cta 644
 Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu
 90 95 100

cag gtg atg cct gac gtg aga ggc att att gcg att ttg ggt gcg aca 692
 Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr
 105 110 115

gcg att gcg att gcc agc cag tat tcc gtg ggg ttg acc ttt ggt ggt 740
 Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly
 120 125 130

gtg atg ggt ccg gtg gtc tct gcg atc gtg acc gtg gct att gat tac 788
 Val Met Gly Pro Val Val Ser Ala Ile Val Thr Val Ala Ile Asp Tyr
 135 140 145

gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa aag cag gaa ttg att 836
 Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile
 150 155 160 165

gat cag ttg att gaa act cgc tcc cag ctg gcg gtg acg gaa cga aat 884
 Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala Val Thr Glu Arg Asn
 170 175 180

gcg ggt att gct gcg gaa cgt caa cgt att gcg cat gaa att cat gac 932
 Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala His Glu Ile His Asp
 185 190 195

acg gtc gcc cag gga ctc tcc tcc att caa atg ctg ctg cat gtc tct 980
 Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met Leu Leu His Val Ser
 200 205 210

gaa cag gag att ctc gtt gct gag atg gaa gag aag cca aag gag gcg 1028
 Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu Lys Pro Lys Glu Ala
 215 220 225

atc gtg aag aag atg cgc ctt gcc cga caa aca gcc tcc gac aat ctc 1076
 Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu
 230 235 240 245

agt gag gct cgc gcg atg att gcg gcg ttg caa ccg gca gcg ctg tct 1124
 Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser
 250 255 260

aaa acc tcc ttg gaa gca gca ctt cac cgc gtc aca gaa ccg ttg ttg 1172
 Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val Thr Glu Pro Leu Leu
 265 270 275

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 Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp Val Arg Gln Leu Pro
 280 285 290
 atg aaa act gaa gcc acc ctt ctg cga att gct caa ggt gcg atc gga 1268
 Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly
 295 300 305
 aat gtg gcg aaa cat tca gag gcg aaa aac tgc cac gtg aca cta acc 1316
 Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr
 310 315 320 325
 tac gaa gac aca gaa gta cgc ctt gat gtg gtt gat gac ggt gtg ggt 1364
 Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly
 330 335 340
 ttt gag cct tcg gaa gtg tcc agt acc ccc gct ggc ctt ggc cat atc 1412
 Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile
 345 350 355
 ggc tta acc gca ttg cag cag cgt gcg atg gaa ttg cac ggc gaa gtt 1460
 Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu Leu His Gly Glu Val
 360 365 370
 ata gtg gaa tct gca tat ggg cag ggt act gcg gta tct gca gca ttg 1508
 Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu
 375 380 385
 ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat 1556
 Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp
 390 395 400 405
 tcg gac tca agt gct aca ggc gag gtt gaa cta agt tct cca act gac 1604
 Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu Ser Ser Pro Thr Asp
 410 415 420
 gat gag taaggctaga ctaaagtacg attcatctgc tcatcgatac tcttgaaggc 1660
 Asp Glu
 gcattttcat tcgaaacgaa gtgcgccatt gggaaggacc tagttcaaac aatgattcgc 1720
 gtgctgcttg ctgatgacca cgaaatcgtg aggctcggac tccgagctgt gctggaaagc 1780
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<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

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AI
 Com. x

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 Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
 35 40 45
 Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
 50 55 60
 His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
 65 70 75 80
 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
 85 90 95
 Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
 100 105 110
 Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
 115 120 125
 Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
 130 135 140
 Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
 145 150 155 160
 Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
 165 170 175
 Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
 180 185 190
 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
 195 200 205
 Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
 210 215 220
 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
 225 230 235 240
 Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
 245 250 255
 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
 260 265 270
 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
 275 280 285
 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
 290 295 300
 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
 305 310 315 320

AI
 Cmt

His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
 325 330 335

Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
 340 345 350

Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 355 360 365

Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 370 375 380

Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
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Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
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Ser Ser Pro Thr Asp Asp Glu
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 <223> Primer luxS-int1

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A1
 Concl.